Loss-of-Function Variants in HOPS Complex Genes *VPS16* and *VPS41* Cause Early Onset Dystonia Associated with Lysosomal Abnormalities

Dora Steel, MD,[1,2†] Michael Zech, MD,[3,4†] Chen Zhao, PhD,[3] Katy E. S. Barwick, PhD,[1] Derek Burke, PhD,[5] Diane Demailly, MD,[6] Kishore R. Kumar, FRACP,[7,8,9,10] Giovanna Zorzi, MD,[11] Nardo Nardocci, MD,[11] Rauan Kaiyrzhanov, MD,[12] Matias Wagner, MD,[3,4] Arcangela Iuso, PhD,[3,4] Riccardo Berutti, PhD,[4] Matej Škorvánek, MD, PhD,[13,14] Ján Necpál, MD,[15] Ryan Davis, PhD,[7,9,10] Sarah Wiethoff, MD, PhD,[16,17] Kshitij Mankad, FRCR,[18] Sniya Sudhakar,[18]

View this article online at wileyonlinelibrary.com. DOI: 10.1002/ana.25879

Received May 12, 2020, and in revised form Jul 31, 2020. Accepted for publication Aug 9, 2020.

Address correspondence to Dr Manju Kurian, NIHR Research Professor and UCL Professor of Neurogenetics, UCL Great Ormond Street Institute of Child Health, 30 Guilford Street, London, WC1N 1EH, United Kingdom. E-mail: manju.kurian@ucl.ac.uk Dr Juliane Winkelmann, Institute of Neurogenomics, Helmholtz Zentrum Munich, Chair of Neurogenetics, Technical University of Munich, TU00000 Technische Universität München, 80333 München, Arcisstr. 21, Germany. E-mail: juliane.winkelmann@tum.de

[†]These authors contributed equally to this work.

From the [1]Department of Developmental Neurosciences, UCL Great Ormond Street Institute of Child Health, London, UK; [2]Department of Neurology, Great Ormond Street Hospital, London, UK; [3]Institute of Neurogenomics, Helmholtz Zentrum München, Munich, Germany; [4]Institute of Human Genetics, Technical University of Munich, Munich, Germany; [5]Enzyme Laboratory, Great Ormond Street Hospital for Children, London, UK; [6]Unités des Pathologies Cérébrales Résistantes, Département de Neurochirurgie, Centre Hospitalier Universitaire, Montpellier, France; [7]Department of Neurogenetics, Kolling Institute of Medical Research, University of Sydney and Northern Sydney Local Health District, Sydney, New South Wales, Australia; [8]Molecular Medicine Laboratory, Concord Repatriation General Hospital, Concord, New South Wales, Australia; [9]Translational Genomics, Kinghorn Centre for Clinical Genomics, Garvan Institute for Medical Research, Sydney, New South Wales, Australia; [10]Department of Neurogenetics, University of Sydney and Northern Sydney Local Health District, Sydney, New South Wales, Australia; [11]Department of Child Neurology, Fondazione IRCCS Istituto Neurologico Carlo Besta, Milan, Italy; [12]Department of Neuromuscular Diseases, University College London, Queen Square, Institute of Neurology, London, UK; [13]Department of Neurology, P. J. Safarik University, Kosice, Slovak Republic; [14]Department of Neurology, University Hospital of L. Pasteur, Kosice, Slovak Republic; [15]Department of Neurology, Zvolen Hospital, Zvolen, Slovakia; [16]UCL Queen Square Institute of Neurology, London, UK; [17]Department of Neurodegenerative Disease, Hertie-Institute for Clinical Brain Research and Center for Neurology, University of Tübingen, Tübingen, Germany; [18]Department of Radiology, Great Ormond Street Hospital for Children, London, UK; [19]Neurology Division, Department of Pediatrics, Lady Hardinge Medical College and Associated Kalawati Saran Children's Hospital, New Delhi, India; [20]Department of Human Genetics, Radboud University Medical Center, Nijmegen, The Netherlands; [21]Department of Neurology, University of Groningen, University Medical Center Groningen, Groningen, The Netherlands; [22]Expertise Center Movement Disorders Groningen, University Medical Center Groningen, Groningen, The Netherlands; [23]Department of Genetics, University of Groningen, University Medical Center Groningen, Groningen, The Netherlands; [24]Department of Neurology, St. George's Hospital, London, UK; [25]Department of Clinical Genetics, St. George's Hospital, London, UK; [26]Genomics England, London, UK; [27]Ken and Ruth Davee Department of Neurology, Northwestern University Feinberg School of Medicine, Chicago, IL, USA; [28]Department of Neurology, St. Vincent's Hospital, Sydney, Australia; [29]Department of Neurology and Clinical Neurophysiology, Children's Health Ireland at Temple Street, Dublin, Ireland; [30]UCD School of Medicine and Medical Science, University College Dublin, Dublin, Ireland; [31]University of Cardiff, Cardiff, Wales, UK; [32]Department of Neurology, Ludwig Maximilian University, Munich, Germany; [33]Department of Neurology, University Medical Center Göttingen, Göttingen, Germany; [34]Department of Neurology and Epileptology, Children's Memorial Health Institute, Warsaw, Poland; [35]Department of Pediatrics and Adolescent Medicine, Division of General Pediatrics, Medical University of Graz, Graz, Austria; [36]Department of Neurology, Medical University Innsbruck, Innsbruck, Austria; [37]Klinik und Poliklinik für Neurologie, Klinikum rechts der Isar, Technische Universität München, Munich, Germany; [38]Department of Neurology, Charles University, 1st Faculty of Medicine and General University Hospital in Prague, Prague, Czech Republic; [39]Genetics and Genomic Medicine, UCL Great Ormond Street Institute of Child Health, London, UK; [40]Department of Neurology, Royal North Shore Hospital, Northern Sydney Local Health District, Sydney, New South Wales, Australia; [41]Department of Histopathology, Great Ormond Street Hospital for Children, London, UK; [42]Lehrstuhl für Neurogenetik, Technische Universität München, Munich, Germany; and [43]Munich Cluster for Systems Neurology, Munich, Germany

Additional supporting information can be found in the online version of this article.

Arianna Ferrini, PhD,[1] Suvasini Sharma, DM,[19] Erik-Jan Kamsteeg, PhD,[20]
Marina A. Tijssen, MD, PhD,[21] Corien Verschuuren, MD,[22,23]
Martje E. van Egmond, MD, PhD,[21,22] Joanna M. Flowers, PhD,[24] Meriel McEntagart, MD,[25]
Arianna Tucci, PhD,[26] Philippe Coubes, MD, PhD,[6] Bernabe I. Bustos, PhD,[27]
Paulina Gonzalez-Latapi, MD,[27] Stephen Tisch, FRACP,[28] Paul Darveniza, FRACP,[28]
Kathleen M. Gorman, MD,[29,30] Kathryn J. Peall, BMBCh, PhD,[31] Kai Bötzel, MD,[32]
Jan C. Koch, MD,[33] Tomasz Kmieć, MD, PhD,[34]
Barbara Plecko, MD, Professor of Pediatrics,[35] Sylvia Boesch, MD,[36]
Bernhard Haslinger, MD,[37] Robert Jech, MD,[38] Barbara Garavaglia, PhD,[11]
Nick Wood, PhD,[16] Henry Houlden, MD,[12] Paul Gissen, MD, PhD,[39] Steven J. Lubbe, PhD,[27]
Carolyn M. Sue, MB.,BS PhD,[7,9,10,40] Laura Cif, MD, PhD,[6] Niccolò E. Mencacci, MD, PhD,[27]
Glenn Anderson, FIBMS,[41] Manju A. Kurian, PhD,[1,2] and Juliane Winkelmann, MD,[3,4,42,43]
Genomics England Research Consortium

Objectives: The majority of people with suspected genetic dystonia remain undiagnosed after maximal investigation, implying that a number of causative genes have not yet been recognized. We aimed to investigate this paucity of diagnoses.
Methods: We undertook weighted burden analysis of whole-exome sequencing (WES) data from 138 individuals with unresolved generalized dystonia of suspected genetic etiology, followed by additional case-finding from international databases, first for the gene implicated by the burden analysis (*VPS16*), and then for other functionally related genes. Electron microscopy was performed on patient-derived cells.
Results: Analysis revealed a significant burden for *VPS16* (Fisher's exact test p value, 6.9×10^{9}). *VPS16* encodes a subunit of the homotypic fusion and vacuole protein sorting (HOPS) complex, which plays a key role in autophagosome-lysosome fusion. A total of 18 individuals harboring heterozygous loss-of-function *VPS16* variants, and one with a microdeletion, were identified. These individuals experienced early onset progressive dystonia with predominant cervical, bulbar, orofacial, and upper limb involvement. Some patients had a more complex phenotype with additional neuropsychiatric and/or developmental comorbidities. We also identified biallelic loss-of-function variants in *VPS41*, another HOPS-complex encoding gene, in an individual with infantile-onset generalized dystonia. Electron microscopy of patient-derived lymphocytes and fibroblasts from both patients with *VPS16* and *VPS41* showed vacuolar abnormalities suggestive of impaired lysosomal function.
Interpretation: Our study strongly supports a role for HOPS complex dysfunction in the pathogenesis of dystonia, although variants in different subunits display different phenotypic and inheritance characteristics.

ANN NEUROL 2020;00:1–14

Dystonia is a common movement disorder associated with significant disability and increased risk of mortality.[1,2] It is characterized by sustained or episodic muscle contractions, which cause abnormal, often repetitive movements and twisting postures affecting the limbs, trunk, neck, and face.[3] Despite significant advances in next-generation sequencing technologies, over 85% of people with suspected genetic dystonia remain undiagnosed after whole-genome sequencing,[4] implying that the majority of genetic dystonias currently remain unrecognized. The reasons for this are multifactorial, attributed to locus heterogeneity, incomplete disease penetrance, and the current limitations of next-generation sequencing technologies.

Here, we report a cohort of individuals with loss-of-function (LOF) mutations in 2 components of the homotypic fusion and vacuole protein sorting (HOPS) complex, a highly conserved complex required for endosome-lysosome and autophagosome-lysosome fusion.[5] We describe a series of patients with generalized dystonia associated with heterozygous LOF variants in *VPS16* and also report biallelic LOF variants in a second HOPS complex gene, *VPS41*, in a child with a severe infant-onset dystonic disorder.

Subjects and Methods

Generalized Dystonia Cohort for Burden Analysis

A consecutive series of 138 unrelated individuals with generalized dystonia (57 men and 81 women, all self-identifying as European) was recruited into the study. Diagnoses were established in accordance with the dystonia consensus criteria[3] at movement disorder specialty centers in Austria, Czechia, and

Germany. The clinical characteristics of the cohort are summarized in Supplementary Table S1. We excluded patients from the cohort who had (i) a known genetic diagnosis or (ii) an acquired form of the disease.

Whole-Exome Sequencing

The generalized dystonia cohort underwent whole-exome sequencing (WES) at the Helmholtz Center Munich (Munich, Germany) according to previously described methods.[6] In brief, the exonic portions of genomic DNA were enriched in solution and indexed with Agilent (Agilent Technologies) SureSelect Human All Exon kits, version 5 and 6. Sequencing was carried out as 100-bp paired-end runs with HiSeq2500/4000 equipment (Illumina). Read processing and variant annotation used an in-house pipeline based on BWA, SAMtools, PINDEL, GATK, ExomeDepth, and custom scripts (Helmholtz Center Munich and Technical University of Munich). Variant filtering was done per standard pipeline analyses, integrating data from online repositories (1000 Genomes Project, gnomAD, dbSNP, ClinVar, and HGMD) and in-house control-exome collections. For the 138 exomes, we obtained on average 13.6 Gb of sequence, resulting in a mean read depth of 143.6-fold with 98.6% of the target nucleotides covered at least 20-fold. Sequences were visualized with IGV. Across the cohort, the exome data were used to exclude causative variants in known disease genes, as described.[6]

Case–Control Rare-Variant Collapsing Analysis (Burden Test)

Gene-based collapsing analysis of rare variants in patients with dystonia versus controls was performed using TRAPD (Test Rare vAriants with Public Data),[7] a robust method for detecting gene-disease associations.[8] We searched for genes with excess mutational burden by comparing genotype counts from 138 generalized dystonia cases with those from gnomAD control subjects (non-Finish European [NFE] cohort, N = 64,603). We coded case and control subjects according to the presence or absence of at least one qualifying variant in any of the ~20,000 consensus coding sequence (CCDS) genes and focused on the following genetic models: (1) dominant LOF, in which qualifying variants were defined as stop-gain, frameshift, and splice-site-altering (± 2 nucleotides of exon boundary) alleles; and (2) dominant non-synonymous, in which qualifying variants were defined as LOF and missense alleles. The minor allele frequency (MAF) threshold of qualifying variants was set at < 0.0005, with the frequency of minor alleles determined from gnomAD (NFE cohort) and ~4,000 non-neurological in-house control exomes for variants present in dystonia case subjects, and in gnomAD (NFE cohort) for variants present in control subjects. To detect differences in the carrier rate of qualifying variants between case and control subjects, we used a one-sided Fisher's exact test. Exome-wide significance was defined at a p value of $< 1.25 \times 10^{6}$, correcting for ~20,000 CCDS genes studied in two individual case-control comparisons. To avoid spurious results, we undertook extensive quality control and harmonization analyses, as described earlier[7,8]: (i) variants overlapping low-complexity regions were filtered out; (ii) sites with a read depth of < 10-fold in either of the 2 cohorts were ignored; and (iii) rare synonymous variant burden testing was conducted. On the basis of the latter, only the top 85% of sites in terms of quality-by-depth (QD) scores for the case sequencing cohort and the top 95% of sites in terms of QD scores for gnomAD were included in the analysis.

Identification of Additional Cases

Using GeneMatcher[9] and direct communications, international collaborators were requested to screen their genomic databases for additional cases. Details of the WES/whole genome sequencing (WGS) methods used differed slightly among each center and can be provided on request. Cases were identified from the UCL Great Ormond Street Institute of Child Health neurogenetic movement disorders cohort (London, UK); the Kolling Institute of Medical Research (Sydney, Australia); the Carlo Besta Neurological Institute (Milan, Italy); the Koios Database of the Queen Square Genomics Group at University College London (London, UK); the Genomics England 100 K Genomes Project dataset (UK), and Radboud University Medical Centre (Nijmegen, The Netherlands). Databases from Cardiff (Wales) and Dublin (Ireland) were also checked but no additional cases were found there. Variants identified through WGS or WES and familial segregation were verified by Sanger sequencing. Details of protocols, reagents, and primer sequences are available on request. All variants are given with reference to the GRCh38 build.

We subsequently undertook a targeted search of the databases above for any additional individuals with mutations affecting other HOPS complex genes not previously associated with disease, namely *VPS18*, *VPS39*, and *VPS41*.

Electron Microscopy

Whole blood samples were obtained in EDTA and centrifuged to produce a buffy coat. Patient fibroblasts were obtained from skin biopsies and cultured in Ham's F10 medium with 12% fetal calf serum. Penicillin and streptomycin were added to the medium for transfer of fibroblasts. Following culture, cells were disaggregated using 0.2% trypsin for microscopy, then centrifuged to form solid clusters. Clusters were fixed in 2.5% glutaraldehyde in 0.1 M cacodylate buffer followed by secondary fixation in osmium tetroxide. Tissues were dehydrated in graded ethanol, transferred to an intermediate reagent, propylene oxide, and then infiltrated and embedded in Agar 100 epoxy resin. Polymerization was undertaken at 60C for 48 hours. Ninety (90) nm ultrathin sections were cut using a Diatome diamond knife on a Leica Ultracut UCT microtome. Sections were transferred to copper grids and stained with alcoholic uranyl acetate and Reynolds lead citrate. The fibroblasts were examined using a JEOL 1400 transmission electron microscope.

Ethics

Ethical approval for genetic research was obtained by each center separately as follows: Great Ormond Street (Family 7): approved by the London Bloomsbury Research Ethics Committee (ref: 13

/LO/0168); Generalized dystonia cohort including Families 1–6: all subjects provided written informed consent, and the study protocol was approved by the institutional ethics review

boards at the Technical University of Munich, Medical University Innsbruck, and Charles University in Prague; Kolling Institute of Medical Research, Northern Sydney Local Health District (Families 8 and 9): reference number RESP/15/314, HREC/15/HAWKE/434; UCL Queen's Square Institute of Neurology, London (Family 10); other families recruited from the Carlos Besta Neurology Institute, Milan (Families 11 and 12); Radboud University Medical Centre, Nijmegen (Family 13); and Genomics England (the 100 K Genomes Project; Family 14) under ethical approval gained by those institutions.

Written informed consent was obtained from patients or their legal guardians for participation with separate consent for publication of recognizable images/videos or invasive procedures, such as skin biopsy where appropriate.

Results

Weighted Burden Analysis and Case Identification

The weighted burden analysis of 138 individuals with etiologically unresolved generalized dystonia (Supplementary Table S1) identified a single study-wide significant signal, *VPS16*, with a Fisher's exact test p value of 6.9×10^{-9} (Fig 1, Supplementary Table S2). In addition to 5 heterozygous LOF alleles uncovered in the burden test (carrier rate of 3.6% in case subjects), we found one individual with a *VPS16*-encompassing microdeletion in the cohort. Through international collaboration, an additional 13 cases with heterozygous LOF variants in *VPS16* were identified. All 19 patients (from 14 families) had *VPS16* variants predicted to result in haploinsufficiency (Table 1, Supplementary Table S3). One proband (Patient 14) had a second, non-truncating *VPS16* variant but phasing of the variants could not be established as parental samples were unavailable. For the other 18 probands, detailed genomic analysis did not identify a second potentially pathogenic *VPS16* variant. Moreover, 9 individuals from 5 multigenerational families (Families 3, 7, 8, 9, and 13) confirmed a clearly dominant pattern of disease inheritance (Fig 2). Segregation analysis was possible in 9 families: of these, de novo occurrence was confirmed in 1 family; inheritance from a symptomatic parent was found in 4 families; and inheritance from an apparently nonmanifesting parent in 4 families, indicating incomplete penetrance.

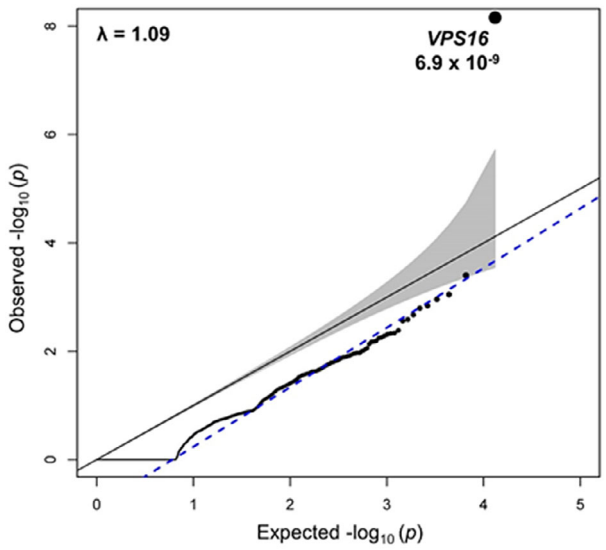

FIGURE 1: Weighted burden analysis. Expected versus observed *p* values of the loss-of-function model are shown for exome-wide gene collapsing analysis in a cohort of 138 individuals with generalized dystonia and gnomAD controls (64,603 non-Finish European subjects). A Fisher's exact test was used to determine differences in the carrier rate of qualifying variants between cases and controls. Qualifying variants were defined as stop-gain, frameshift, and essential splice-site variants with a minor allele frequency of < 0.0005, whereas exome-wide significance was set to a *p* value of $< 1.25 \times 10^{-6}$ (Bonferroni-corrected threshold, see Methods). We observed a significant mutational burden (minimal genomic inflation) for *VPS16*, in which 5 individuals with dystonia had a qualifying variant. The signal and corresponding Fisher's exact test *p* value for *VPS16* is indicated. [Color figure can be viewed at www.annalsofneurology.org]

Clinical Features of Patients With VPS16

Affected individuals presented with a progressive early onset dystonia (median age 12 years, range 3–50 years), with prominent oromandibular, bulbar, cervical, and upper limb involvement (Fig 3A, Tables 2 and 3). Progressive generalization ensued in most cases, although most remained ambulant, and only a minority (16%) lost the ability to walk in adulthood (Supplementary Videos S1–S3). Additional clinical features of mild to moderate intellectual disability and neuropsychiatric symptoms were present in approximately one-third of patients, and 50% of families had a positive family history of dystonia (Supplementary Table S4). A degree of interfamilial and intrafamilial phenotypic variability was evident, both with regard to age of symptom onset and dystonia severity. Routine diagnostic testing was unremarkable. In 4 individuals, magnetic resonance imaging (MRI) showed bilateral and symmetrical hypointensity of the globi pallidi and sometimes also the midbrain and dentate nuclei on MRI sequences known to demonstrate susceptibility (T2-weighted, T2*-weighted, and susceptibility-weighted datasets), suggestive of iron deposition.[10] Mild generalized cerebral atrophy was also apparent in 4 individuals. Although not grossly abnormal, caudate nuclei and putamina appeared relatively small and bright on T2 (Fig 3B, see Supplementary Table S4). Some patients had a partial response to levodopa, trihexyphenidyl, and/or botulinum toxin type A injections. Deep-brain stimulation was also beneficial for some, but not all patients; sustained improvement in motor and disability scores for the Burke-Fahn-Marsden Dystonia Rating Scale were observed for Patient 7C (Supplementary Video S4, Supplementary Table S5).

TABLE 1. Genomic Characteristics of *VPS16* Variants Identified

Genomic position	cDNA variant	Effect on protein	Variant type	Family number
chr20:2835462–3974387	NA	Microdeletion	CNV	6
chr20:2860515	c.436del	p.Ile146Serfs*65	Frameshift	9
chr20:2860534–2860541	c.455_462dup	p.Leu155Alafs*59	Frameshift	13
chr20:2860792	c.559C > T	p.Arg187*	Stop-gain	4, 10
chr20:2862601–2862602	c.1094_1095dup	p.Tyr366Serfs*12	Frameshift	7
chr20:2863068	c.1335 T > G	p.Tyr455*	Stop-gain	3
chr20:2863102	c.1367 + 2 T > C	p.?	Splice site loss	8
chr20:2864178	c.1612-1G > C	p.?	Splice site loss	14
chr20:2864288	c.1720 + 1G > C	p.?	Splice site loss	11
chr20:2864631	c.1903C > T	p.Arg635*	Stop-gain	1, 2, 12
chr20:2865039–2865040	c.1988_1989insG	p.Asn663Lysfs*2	Frameshift	5

CNV = copy number variant; NA = all variants are described with reference to build GRCh38, transcript NM_022575.3.

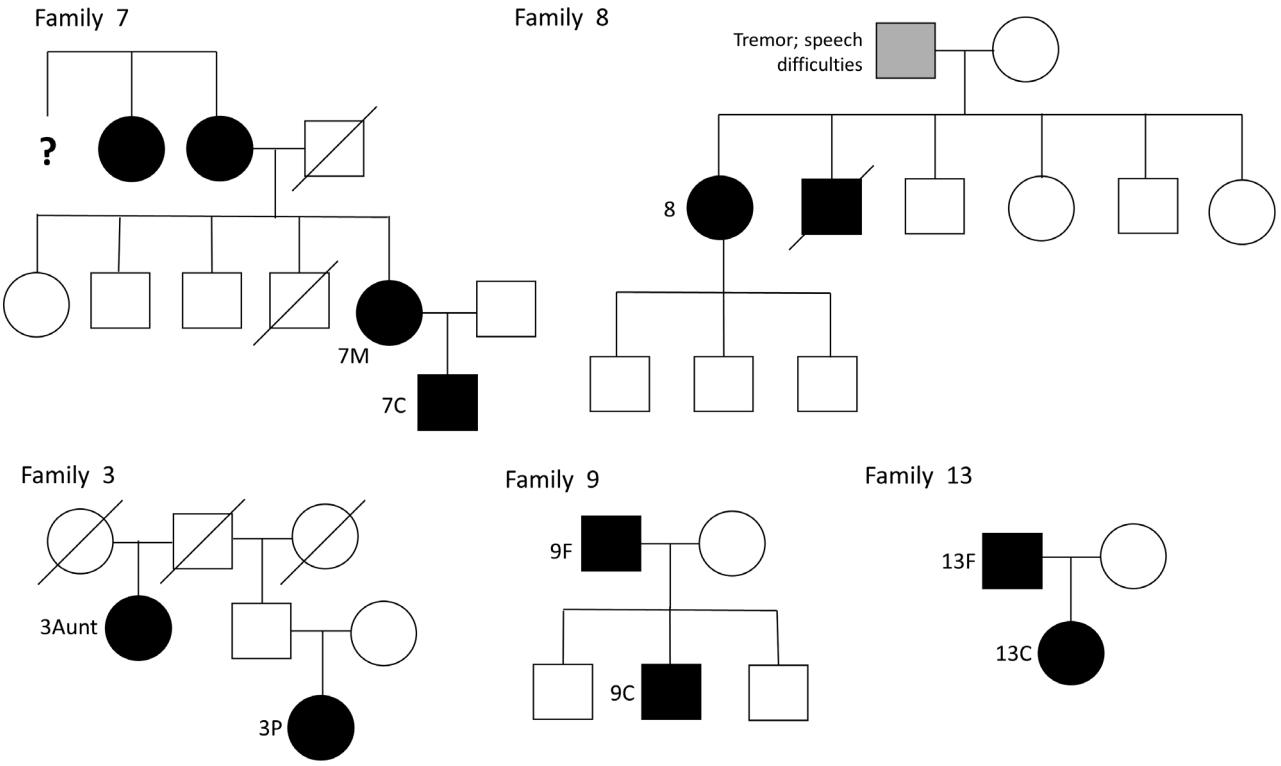

FIGURE 2: Pedigrees of families affected by *VPS16* dystonia, showing autosomal dominant inheritance. Key: circle = female; square = male; black-filled shape = individual affected by dystonia; grey-filled shape = individual may have been affected by dystonia; diagonal slash = individual deceased; ? = number/status of additional siblings not known.

Identification and Characterization of Individuals With Biallelic VPS41 *Variants*

Screening databases for potentially pathogenic variants in HOPS complex genes not previously implicated in disease (*VPS18*, *VPS39*, and *VPS41*) identified one proband from a consanguineous family with a homozygous canonical splicing variant (NM_014396.3:c.450 + 1G > T) in *VPS41*, resulting in exon 7 skipping and loss of 22 amino acid

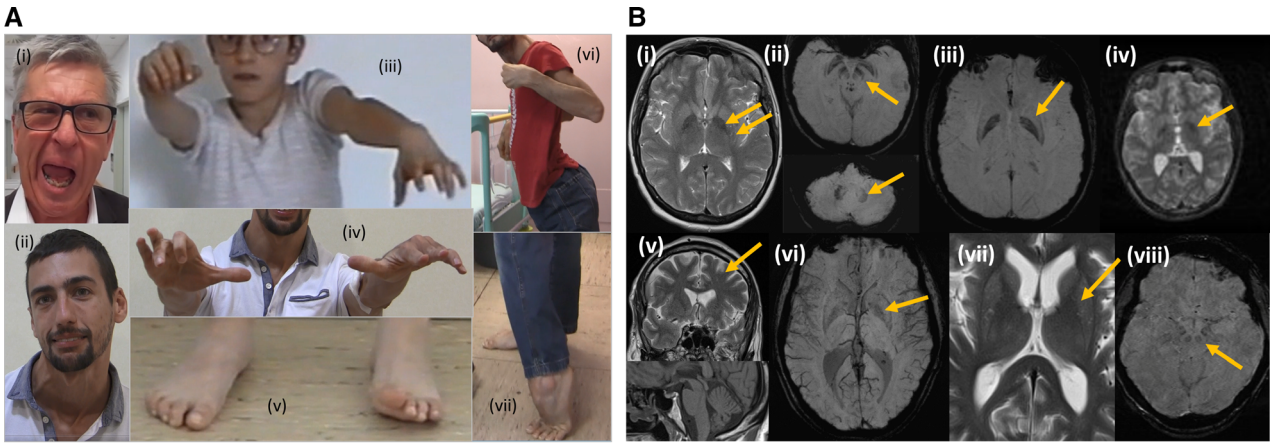

FIGURE 3: Clinical photographs showing dystonic posturing in *VPS16* patient cohort. (A) (i) Patient 9 F demonstrating orofacial dystonia elicited during speech; (ii) Patient 11 S1 showing cervical dystonia; (iii) Patient 12 showing upper limb posturing; (iv) Patient 11 S1 showing hand posturing; (v) Patient 12 showing spontaneous striatal toe on the left; (vi) Patient 12 as an adult, standing, showing exaggerated lumbar lordosis; and (vii) Patient 12 as an adult, standing, showing involuntary plantar flexion/tiptoe posture. (B) Selected MRI brain images for patients with *VPS16* dystonia. Abnormalities indicated by white arrows. (i) Axial T2 image from Patient 7 M (aged 34 years, pre-DBS) shows hypointensity consistent with iron deposition in the globi pallidi; (ii) susceptibility-weighted images (SWIs) from Patient 7 M showing hypointensity in the midbrain nuclei (above) and dentate nucleus of the cerebellum (below); (iii) axial SWI from Patient 7 M showing hypointensity of the globi pallidi; (iv) axial T2 image from Patient 1 (aged 10 years) showing hypointensity of the globi pallidi; (v) subtle generalized atrophy in Patient 9 F, demonstrated in a coronal T2 image of the cerebrum (above) and a sagittal T1 image of the cerebellum (below); (vi) axial SWI from Patient 10, aged 32 years, showing hypointensity in the globi pallidi; (vii) enlarged axial T2 image from Patient 13 F, aged 55 years, showing relatively small, bright caudates, and putamina; and (viii) axial SWI image from Patient 3 P (aged 21 years) showing hypointensity of the midbrain nuclei. [Color figure can be viewed at www.annalsofneurology.org]

residues (p.Ile129_Lys150del; Fig 4). This patient presented in infancy with global developmental delay and generalized dystonia. He attained a few words of speech and voluntary limb movements but never sat unsupported. He had pale optic discs and an axonal neuropathy. From 6 years of age, his condition began to deteriorate, with reduced motor abilities and alertness. An MRI of the brain showed atrophy of the superior cerebellar vermis and slimming of the posterior limb of the corpus callosum (Fig 4).

Electron Microscopy

Electron microscopy (EM) was performed on patient-derived fibroblasts and peripheral lymphocytes from patients with both *VPS16* and *VPS41* mutations in order to determine the impact on lysosomal and vacuolar morphology. When compared to age-matched controls, *VPS16* patient cells (fibroblasts n = 6; and lymphocytes n = 4) contained increased clusters of vacuoles, with some containing inclusions in the form of particulate or laminated material (Fig 5, see Supplementary Fig S1). EM analysis of patient-derived fibroblasts and lymphocytes from the patient with *VPS41* showed numerous membrane-bound vacuoles containing granular material and, in some cases, fine electron-dense laminated strands. A large number of small pinocytic vesicles arising from the plasma membrane were also seen. In both *VPS16*-related and *VPS41*-related disease, the EM changes seen in patient-derived tissue were consistent with lysosomal dysfunction.

Discussion

We report a cohort of 20 individuals with mutations in 2 related genes, *VPS16* and *VPS41*, which encode vacuolar protein sorting-associated proteins 16 and 41, respectively, both key components of the HOPS complex. The HOPS complex mediates autophagosome-lysosome and endosome-lysosome fusion through several different interactions with SNARE proteins, including catalyzing the formation of the SNARE complex[11] and protection of the trans-SNARE complex from disassembly once formed (Fig 6).[12]

Our observation of incomplete penetrance in *VPS16*-related disease (a common hindrance to gene discovery) suggests that, like most other genetic dystonias,[13] additional genetic, epigenetic, and/or environmental factors are likely to play an important role in disease manifestation. Indeed, weighted burden analysis suggests a wider role for *VPS16* in conferring genetic susceptibility in a broader group of patients with dystonia. Although adolescent-onset dystonia has been reported in a single family harboring a homozygous missense mutation in *VPS16*,[14] our data suggest that *VPS16* haploinsufficiency (dominant inheritance with incomplete penetrance) is a much more common genetic mechanism for *VPS16*-related disease.

Autosomal dominant *VPS16*-related disease appears to be an early-onset, progressively generalizing dystonia,

TABLE 2. Probands' Variants and Demographic Characteristics

Family	Patient	Mutation	Inheritance*	Sex	Current age, yr
1	1	p.Arg635*	NK	M	27
2	2	p.Arg635*	NK	F	42
3	3P	p.Tyr455*	I-AP	F	24
	3Aunt			F	50
4	4	p.Arg187*	I-AP	M	26
5	5	p.Asn663 Lysfs*2	NK	M	38
6	6	Micro-deletion: chr20:2835462–3974387	DN	F	21
7	7 M	p.Tyr366 Serfs*12	I-SP	F	45
	7C			M	26
8	8	c.1367 + 2 T > C	I-SP	F	69
9	9F	p.Ile146 Serfs*65	I-SP	M	62
	9C			M	30
10	10	p.Arg187*	NK	M	32
11	11S1	c.1720 + 1 G > C	I-AP	M	30
	11S2			M	24
12	12	p.Arg635*	I-AP	M	33
13	13F	p.Leu155Alafs*59	I-SP	M	58
	13C			F	17
14	14	c.1612–1 G > C	NK	M	57

Patient identifiers: XC = child; XF = father; XM = mother; XP = proband; XS = sibling.
DN = de novo; F = female; I-AP = inherited from asymptomatic parent; I-SP = inheritance from symptomatic parent; M = male; NK = not known.
*For multigenerational families, inheritance refers to the younger affected generation.

which may occur in isolation or in combination with neuropsychiatric and neurodevelopmental features. In this study, it clinically resembles other "classic" genetic dystonias, such as those related to *KMT2B* or *TOR1A*: indeed, at least 1 family (Family 7) in our study had initially been referred for *KMT2B* testing. Radiologically, too, there is a degree of overlap with *KMT2B* disease, with basal ganglia hypointensity seen on T2 (and other related MRI sequences) in a proportion of patients[15]: whether this reflects a common pathophysiological mechanistic end point remains to be determined. Our series does not identify any therapeutic option as reliably beneficial for all patients with *VPS16*-related disease but it is notable that some patients did derive significant benefit from deep brain stimulation (DBS), a treatment that has also proved very useful for both *TOR1A* and *KMT2B*-affected patients. Three patients also reported some degree of levodopa responsivity, which, although far from conclusive, may be worth pursuing for mutation-positive patients.

There are clear differences between *VPS16*-related and *VPS41*-related disease, although both involve subunits of the HOPS complex and manifest with dystonia as a prominent symptom. Whereas the cases of *VPS16*-related dystonia we report involve monoallelic variants, predicted to cause haploinsufficiency, the child with *VPS41*-related disease has biallelic LOF mutations. He also has a correspondingly more profound phenotype, with very early onset of symptoms (presentation in infancy compared to the *VPS16* patient cohort, median age of presentation 12 years), severe neurodevelopmental impairment, and evidence of clinical deterioration from during childhood. The differing MRI findings (cerebellar vermis atrophy in *VPS41* vs subtle basal ganglia changes in *VPS16*) also

TABLE 3. Features of Probands' Dystonia

Patient	Age of dystonia onset, yr	Initial movement disorder	Current movement disorder				
			Axial	Limb	Facial/ bulbar	Ambulant?	Helpful interventions
1	10	Cervical dystonia	Y	Y (R > L)	Y (severe speech involvement)	Y	DBS (partial improvement)
2	13	Writer's cramp	Y (mild)	Y (U > Lo)	N	Y	N
3 P	17	Upper limb dystonia (R)	Y	Y	Y (severe speech involvement)	N (lost in adulthood)	N
3 Aunt	4	Upper limb dystonia (R)	Y	Y (U only)	Yes (speech involvement)	Y	Levodopa (minor improvement); sensory trick
4	15	Speech involvement then cervical dystonia	Y	Y (U only)	Y	Y	N
5	30	Cervical dystonia	Y	Y (U only)	Y	Y	N
6	11	Upper limb dystonia (R)	Y	Y (U > Lo)	Y	Y	N
7 M	19	Lower limb dystonia (R)	Y	Y	Y	N (lost in adulthood)	DBS (significant improvement)
7 C	11	Facial + cervical dystonia	Y	Y (mild; U > Lo)	Y	Y (with difficulty)	DBS (significant improvement)
8	7	Cervical + upper + lower limb (R) dystonia	Y	Y (U and Lo)	Y (marked dysphonia)	Y	Levodopa; Botox Sensory trick
9 F	14	Oromandibular dystonia	Y (cervical)	Y (U and Lo)	Y (dysphonia; blepharospasm)	Y	Levodopa; Botox Sensory trick
9 C	Unknown	Oromandibular dystonia	Y (cervical)	N	Y (blepharospasm; oromandibular)	Y	N
10	19	Oromandibular dystonia	Y (cervical)	Y (mild; U only)	Y (laryngeal)	Y	TXY; Botox Sensory trick
11 S1	8	Writer's cramp	Y (cervical)	Y (U > Lo)	Y (severe dysphonia)	Y	Botox (larynx)
11 S2	7	Writer's cramp	N	Y (Lo > U)	Y (dysphonia; oromandibular)	Y	N (DBS no use)
12	3	Speech involvement	Y	Y	Yes (anarthria)	N (lost age 20y)	N (DBS no use)
13 F	50	Cervical dystonia	Y	Y (U > Lo)	N	Y (with difficulty)	
13 C	9	Lower limb dystonia (R)	N	Y	N	Y	TXY
14	14	Cervical dystonia + speech involvement	Y	Y (U > Lo)	Y	Y	Botox Sensory trick

Botox = botulinum toxin type A; DBS = deep brain stimulation; L = left; Lo = lower; R = right; TXY = trihexyphenidyl; U = upper.

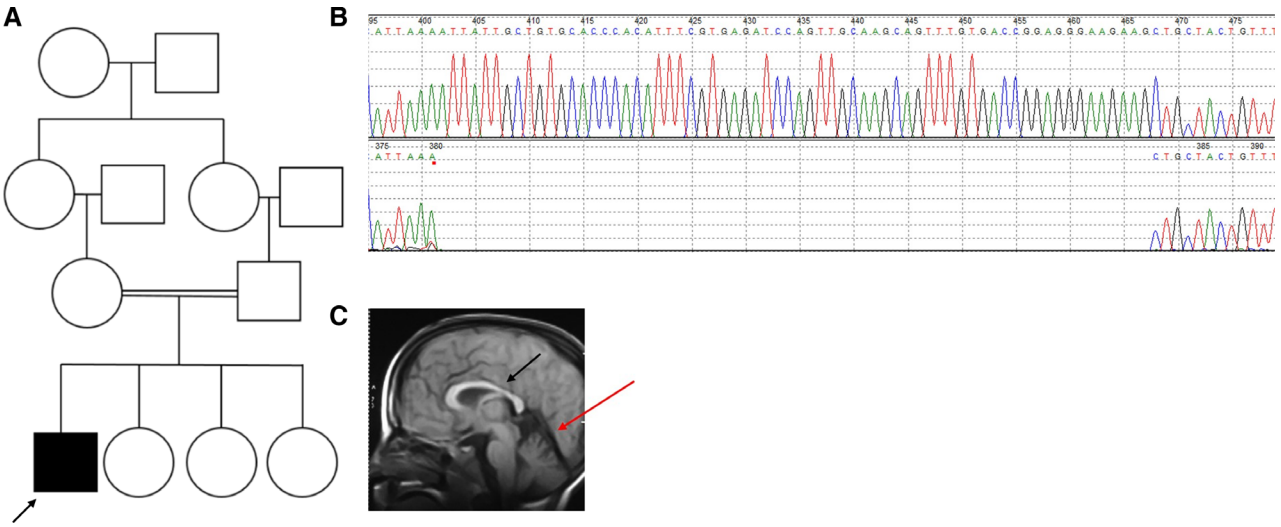

FIGURE 4: Features of proband with *VPS41*-related condition. (A) Pedigree of the *VPS41* patient's family: the proband is indicated with an arrow. Key: circle = female; square = male; filled shape = affected individual; double horizontal line = consanguineous union. (B) Sequencing chromatogram for cDNA of *VPS41*: top row shows wild-type reference sequence and second row shows results from Sanger sequencing of patient cDNA. Bases corresponding to Exon 7 are absent in the patient. (C) T2-weighted midline sagittal MRI brain scan from *VPS41* proband. Note thinning of posterior aspect of corpus callosum (*black arrow*) and atrophy of superior cerebellar vermis (*white arrow*). [Color figure can be viewed at www.annalsofneurology.org]

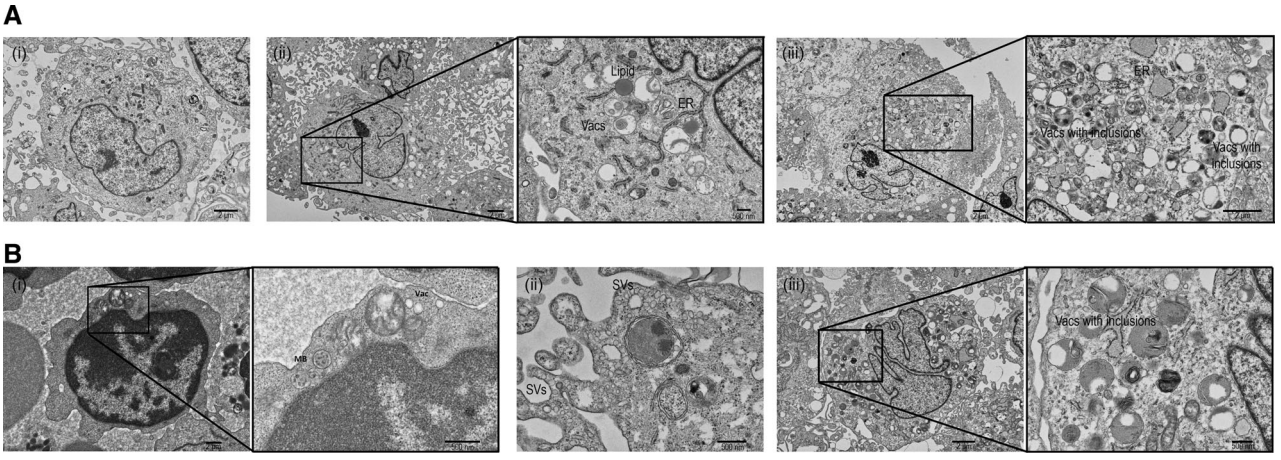

FIGURE 5: Representative electron microscopy images of patient-derived and control cells. (A) (i) Control fibroblast from a healthy individual. (ii) From Patient 8; (iii) from Patient 11 S2; black rectangles in (ii) and (iii) indicate the region enlarged in the following image. (B) Representative electron microscopy images of *VPS41* patient-derived cells. (i) Lymphocyte, showing small vacuoles and multivesicular bodies; (ii) fibroblast showing numerous small intracellular and membrane-abutting vesicles; (iii) fibroblast showing vacuoles containing inclusions. Black rectangles in (i) and (iii) indicate the region enlarged in the following image. ER = endoplasmic reticulum; MB = multivesicular bodies; SVs = small vesicles PV: pinocytic vesicles; Vacs = vacuoles.

suggest some divergence of pathophysiological pathways. Corroborating our findings, we note that a paper not yet published but recently deposited with bioRxiv describes an additional family where 2 siblings with homozygous missense variants in *VPS41* were affected by dystonia and ataxia, with similar MRI findings to our proband, and lysosomal abnormalities in patient-derived fibroblasts.[16] Thus, our study further supports the emerging role of biallelic LOF *VPS41* mutations in early-onset movement disorders.

The microscopic vacuolar changes we observed in both *VPS16* and *VPS41*-patient-derived cells are consistent with lysosomal dysfunction. Vacuolar changes have also been observed in fibroblasts from patients with mucopolysaccharidosis-plus syndrome due to biallelic variants in *VPS33A*, another subunit of the HOPS complex.[17] These observations are in keeping with in vitro studies on human cell lines, where depletion of both *VPS16*[18] and *VPS41*[19] have been separately shown to impair endosomal-lysosomal fusion. Furthermore, the accumulation of vacuoles has been observed in *Drosophila* pigment cells in a *dVps16A* knockdown model[20] and yeast cells expressing mutant *vps41* protein are reported to contain many small membrane-bound compartments.[21] It has been suggested

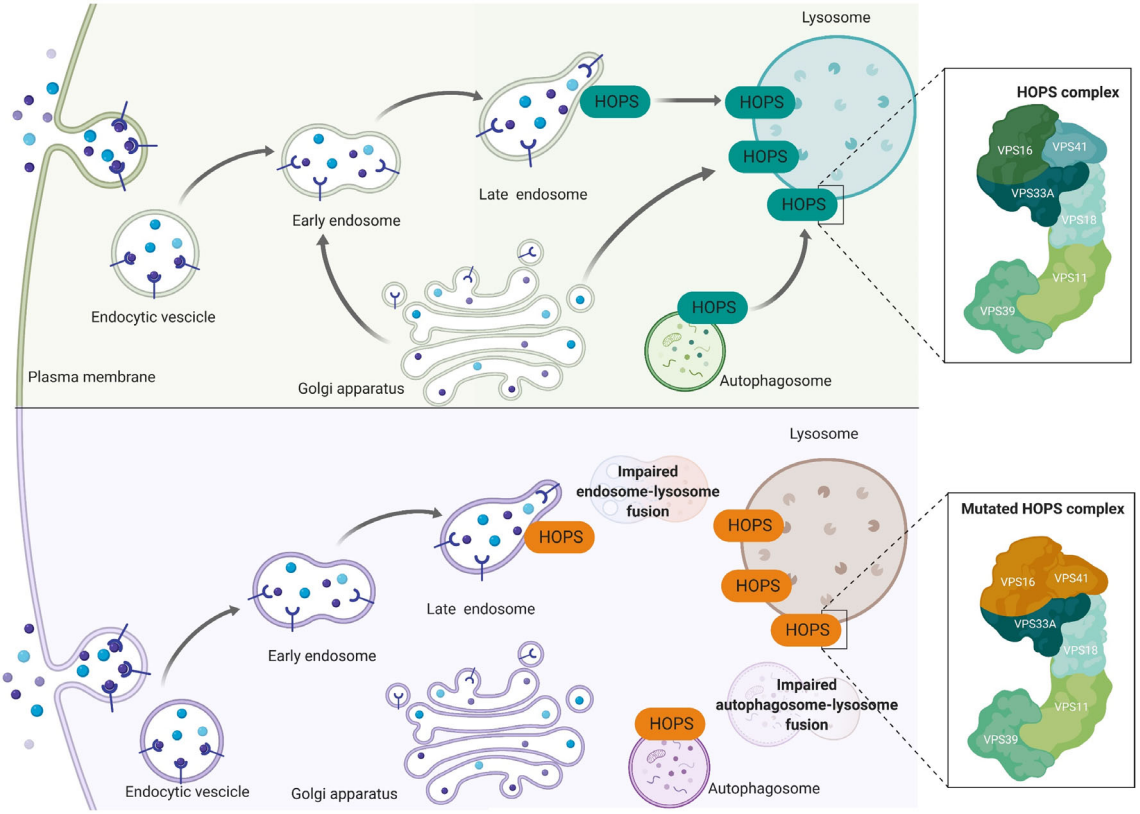

FIGURE 6: Schematic showing the role of the HOPS complex (right) in fusion of endosomes and autophagosomes with lysosomes, in health (above) and disease (below). [Color figure can be viewed at www.annalsofneurology.org]

that *VPS41*, through its contribution to autophagocytosis, plays a role in suppression of neurodegenerative processes, especially those mediated by toxic accumulation of aberrant proteins: overexpression of human *VPS41* has been shown to be protective in *Caenorhabditis elegans* models of both Parkinson's[22] and Alzheimer's diseases.[23]

Although other components of the HOPS complex have been reported in human disease (specifically *VPS33A* in mucopolysaccharidosis-plus syndrome[17] and *VPS11* in hypomyelinating leukodystrophy type 12)[24] unlike *VPS16* and *VPS41*, none have been associated with dystonia phenotypes, thereby identifying a new pathway in dystonia pathogenesis. We postulate that impairment of endosomal-lysosomal fusion may hinder key cellular processes within core neural networks governing motor control (see Fig 6). Overall, our study provides compelling evidence for the role of *VPS16* and *VPS41* in the physiological control of movement, mediated through its role in the HOPS complex and lysosomal function.

Acknowledgments

The authors would like to thank the patients and their families who took part in our study.

Financial Support

This study was funded by a research grant from the Else Kröner-Fresenius-Stiftung as well as by in-house institutional funding from Technische Universität München, Munich, Germany, Helmholtz Zentrum München, Munich, Germany, Medizinische Universität Innsbruck, Innsbruck, Austria, and Charles University, Prague, Czech Republic (PROGRES Q27). This study was also funded by the Czech Ministry of Education under grant AZV: NV19-04-00233 and under the frame of EJP RD, the European Joint Programme on Rare Diseases (EJP RD COFUND-EJP No. 825575), as well as the Slovak Grant and Development Agency under contract APVV-18-0547 and the Slovak Research and Grant Agency under contract number VEGA 1/0596/19 to M.S. M.A.K. and D.S. are funded by a National Institute for Health Research (NIHR) Research Professorship. M.A.K.'s research group also benefits from funding from the Sir Jules Thorn Trust and Rosetrees Trust. M.Z. was supported by an internal research program at Helmholtz Zentrum München, Munich, Germany ("Physician Scientists for Groundbreaking Projects"). K.R.K. is supported by a research award from the Aligning Science Across Parkinson's initiative, Michael J. Fox Foundation, as well as a donation

through the Paul Ainsworth Family Foundation. S.W. is supported by the Ministry of Science, Research and the Arts of Baden-Württemberg, and the European Social Fund (ESF) of Baden-Württemberg (31-7635 41/67/1). CMS is a National Health and Medical Research Council Practitioner Fellow (#1136800). M.A.T. reports grants from The Netherlands Organisation for Health Research and Development ZonMW Topsubsidie (91218013), the European Fund for Regional Development from the European Union (01492947), and the province of Friesland, Dystonia Medical Research Foundation, from Stichting Wetenschapsfonds Dystonie Vereniging, from Fonds Psychische Gezondheid, from Phelps Stichting, and an unrestricted grants from Actelion and AOP Orphan Pharmaceuticals AG.

This research was made possible through access to the data and findings generated by the 100,000 Genomes Project. The 100,000 Genomes Project is managed by Genomics England Limited (a wholly owned company of the Department of Health and Social Care). The 100,000 Genomes Project is funded by the National Institute for Health Research and NHS England. The Wellcome Trust, Cancer Research UK, and the Medical Research Council have also funded research infrastructure. The 100,000 Genomes Project uses data provided by patients and collected by the National Health Service as part of their care and support.

Author Contributions

M.A.K., J.W., D.S., and M.Z. contributed to the conception and design of the study. D.S., M.Z., C.Z., K.E.S.B., D.B., D.D., K.R.K., G.Z., N.N., R.K., M.W., A.I., R.B., M.S., J.N., R.D., S.W., K.M., S.S., A.F., S.Sh., E.J.K., M.A.T., C.V., M.E.v.E., J.M.F., M.M., A.T., P.C., B.I.B., P.G.L., S.T., P.D., K.M.G., K.J.P., K.B., J.C.K., T.K., B.P., S.B., B.H., B.G., R.J., N.W., H.H., P.G., S.J.L., C.M.S., L.C., N.E.M., G.A., M.A.K., and J.W. contributed to the acquisition and analysis of data. D.S., M.Z., M.A.K., J.W., C.Z., G.A., A.F., K.M., and S.S. contributed to drafting the text and preparing the figures.

Author Name	Contribution
Dora Steel	Genomic analysis; clinical data acquisition and analysis, compilation of data; drafting manuscript
Michael Zech	Genomic analysis; undertaking burden analysis; clinical data acquisition and analysis; compilation of data; drafting manuscript
Chen Zhao	Undertaking burden analysis; Preparation of images in the manuscript
Katy E. S. Barwick	Undertook splicing impact experiments for VPS41-related work
Derek Burke	Culture and preparation of patient-derived cells for electron microscopy
Diane Demailly	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Kishore R. Kumar	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Giovanna Zorzi	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript; acquisition and processing of patient samples
Nardo Nardocci	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Rauan Kaiyrzhanov	Interrogation of genomic datasets; case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Matias Wagner	Genomic analysis; compilation of genetic data
Arcangela Iuso	Genomic analysis; compilation of genetic data
Riccardo Berutti	Genomic analysis; compilation of genetic data
Matej Škorvánek	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript, and with detailed phenotyping of probands in the burden analysis case cohort used in this study
Ján Necpál	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript, and with detailed phenotyping of probands in the burden analysis case cohort used in this study
Ryan Davis	Acquisition and preparation of patient samples including fibroblast culture for electron microscopy

Sarah Wiethoff	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Kshitij Mankad	Analysis, selection and presentation of radiological data and images
Sniya Sudhakar	Analysis, selection and presentation of radiological data and images
Arianna Ferrini	Interrogation of related genomic/clinical datasets and genetic/clinical data analysis
Suvasini Sharma	Case contribution (VPS41), with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript; obtaining and processing patient tissue samples
Erik-Jan Kamsteeg	Interrogation of genomic datasets; case contribution, analysis of genetic and clinical data in the manuscript
Marina A. Tijssen	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Corien Verschuuren	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript; acquisition and processing of patient samples
Martje E. van Egmond	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Joanna M. Flowers	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Meriel McEntagart	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Arianna Tucci	Data analysis and preparation of images in the manuscript
Philippe Coubes	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Bernabe I. Bustos	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Paulina Gonzalez-Latapi	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Stephen Tisch	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Paul Darveniza	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Kathleen M. Gorman	Interrogation of related genomic and clinical datasets
Kathryn J. Peall	Interrogation of related genomic and clinical datasets
Kai Bötzel	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Jan C. Koch	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Tomasz Kmieć	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Barbara Plecko	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Sylvia Boesch	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript, and with detailed phenotyping of probands in the burden analysis case cohort used in this study
Bernhard Haslinger	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript, and with detailed phenotyping of probands in the burden analysis case cohort used in this study
Robert Jech	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript, and with detailed phenotyping of probands in the burden analysis case cohort used in this study;

	acquisition and processing of patient samples
Barbara Garavaglia	Acquisition and preparation of patient samples including fibroblast culture for electron microscopy
Nick Wood	Acquisition, management and interrogation of genomic datasets
Henry Houlden	Acquisition, management and interrogation of genomic datasets
Paul Gissen	Input on the scientific and theoretical aspects of HOPS gene biology, with conception of electron microscopy experiments relevant to this study
Steven J. Lubbe	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Carolyn M. Sue	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Laura Cif	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Niccolò E. Mencacci	Case contribution, with detailed clinical endophenotyping of proband and family members and analysis of clinical data in the manuscript
Glenn Anderson	Acquisition, detailed analysis and presentation of electron microscopy images
Manju A. Kurian	Project conceptualisation, leadership and coordination; data analysis and validation, manuscript preparation
Juliane Winkelmann	Project conceptualisation, leadership and coordination; data analysis and validation, manuscript preparation

Potential Conflicts of Interest

None of the authors has any relevant conflict of interest to declare.

URLs

CADD (Combined Annotation Dependent Depletion): https://cadd.gs.washington.edu/snv
gnomAD: https://gnomad.broadinstitute.org/
MutationTaster: http://www.mutationtaster.org/
PROVEAN: http://provean.jcvi.org/index.php

References

1. Balint B, Mencacci NE, Valente EM, et al. Dystonia. Nat Rev Dis Primers 2018;4:25.
2. Lumsden DE, King MD, Allen NM. Status dystonicus in childhood. Curr Opin Pediatr 2017;29:674–682.
3. Albanese A, Bhatia K, Bressman SB, et al. Phenomenology and classification of dystonia: a consensus update. Mov Disord 2013;28:863–873.
4. Kumar KR, Davis RL, Tchan MC, et al. Whole genome sequencing for the genetic diagnosis of heterogenous dystonia phenotypes. Parkinsonism Relat Disord 2019;69:111–118.
5. Jiang P, Nishimura T, Sakamaki Y, et al. The HOPS complex mediates autophagosome-lysosome fusion through interaction with syntaxin 17. Mol Biol Cell 2014;25:1327–1337.
6. Zech M, Boesch S, Jochim A, et al. Clinical exome sequencing in early-onset generalized dystonia and large-scale resequencing follow-up. Mov Disord 2017;32:549–559.
7. Guo MH, Plummer L, Chan YM, et al. Burden testing of rare variants identified through exome sequencing via publicly available control data. Am J Hum Genet 2018;103:522–534.
8. Ulirsch JC, Verboon JM, Kazerounian S, et al. The genetic landscape of diamond-Blackfan anemia. Am J Hum Genet 2018;103:930–947.
9. Sobreira N, Schiettecatte F, Valle D, Hamosh A. GeneMatcher: a matching tool for connecting investigators with an interest in the same gene. Hum Mutat 2015;36:928–930.
10. Pietracupa S, Martin-Bastida A, Piccini P. Iron metabolism and its detection through MRI in parkinsonian disorders: a systematic review. Neurol Sci 2017;38:2095–2101.
11. Orr A, Song H, Rusin SF, et al. HOPS catalyzes the interdependent assembly of each vacuolar SNARE into a SNARE complex. Mol Biol Cell 2017;28:975–983.
12. Xu H, Jun Y, Thompson J, et al. HOPS prevents the disassembly of trans-SNARE complexes by Sec17p/Sec18p during membrane fusion. EMBO J 2010;29:1948–1960.
13. Camargos S, Cardoso F. Understanding dystonia: diagnostic issues and how to overcome them. Arq Neuropsiquiatr 2016;74:921–936.
14. Cai X, Chen X, Wu S, et al. Homozygous mutation of VPS16 gene is responsible for an autosomal recessive adolescent-onset primary dystonia. Sci Rep 2016;6:25834.
15. Meyer E, Carss KJ, Rankin J, et al. Mutations in the histone methyltransferase gene KMT2B cause complex early-onset dystonia. Nat Genet 2017;49:223–237.
16. van der Welle REN, Jobling R, Burns C, et al. VPS41 recessive mutation causes ataxia and dystonia with retinal dystrophy and mental retardation by inhibiting HOPS function and mTORC1 signaling. bioRxiv 2019. Preprint https://www.biorxiv.org/content/10.1101/2019.12.18.867333v1.full.pdf.
17. Pavlova EV, Shatunov A, Wartosch L, et al. The lysosomal disease caused by mutant VPS33A. Hum Mol Genet 2019;28:2514–2530.
18. Wartosch L, Günesdogan U, Graham SC, Luzio JP. Recruitment of VPS33A to HOPS by VPS16 is required for lysosome fusion with endosomes and Autophagosomes. Traffic 2015;16:727–742.
19. Pols MS, ten Brink C, Gosavi P, et al. The HOPS proteins hVps41 and hVps39 are required for Homotypic and heterotypic late endosome fusion. Traffic 2012;14:219–232.

20. Pulipparacharuvil S, Akbar MA, Ray S, et al. Drosophila Vps16A is required for trafficking to lysosomes and biogenesis of pigment granules. J Cell Sci 2005;118:3663–3673.

21. Radisky DC, Snyder WB, Emr SD, Kaplan J. Characterization of VPS41, a gene required for vacuolar trafficking and high-affinity iron transport in yeast. Proc Natl Acad Sci U S A 1997;94:5662–5666.

22. Ruan Q, Harrington AJ, Caldwell KA, et al. VPS41, a protein involved in lysosomal trafficking, is protective in Caenorhabditis elegans and mammalian cellular models of Parkinson's disease. Neurobiol Dis 2010;37:330–338.

23. Griffin EF, Yan X, Caldwell KA, Caldwell GA. Distinct functional roles of Vps41-mediated neuroprotection in Alzheimer's and Parkinson's disease models of neurodegeneration. Hum Mol Genet 2018;27: 4176–4193.

24. Edvardson S, Gerhard F, Jalas C, et al. Hypomyelination and developmental delay associated with VPS11 mutation in Ashkenazi-Jewish patients. J Med Genet 2015;52:749–753.